

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
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Application Serial Number: 09/937,495  
Source: I FW/6  
Date Processed by STIC: 2-2-05

***ENTERED***



IFW16

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/937,495

DATE: 02/02/2005  
TIME: 16:16:49

Input Set : E:\seqlist.txt  
Output Set: N:\CRF4\02022005\I937495.raw

3 <110> APPLICANT: KUSUNOKI, CHIHIRO  
4 FUKUSHIMA, ATSUSHI  
6 <120> TITLE OF INVENTION: METHOD FOR PREPARING MONOCLOINAL ANTIBODY  
8 <130> FILE REFERENCE: SHIM-013  
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/937,495  
C--> 11 <141> CURRENT FILING DATE: 2002-02-28  
11 <150> PRIOR APPLICATION NUMBER: JP11-087929  
12 <151> PRIOR FILING DATE: 1999-03-30  
14 <150> PRIOR APPLICATION NUMBER: JP00/02022  
15 <151> PRIOR FILING DATE: 2000-03-30  
17 <160> NUMBER OF SEQ ID NOS: 5  
19 <170> SOFTWARE: PatentIn Ver. 2.1  
21 <210> SEQ ID NO: 1  
22 <211> LENGTH: 1507  
23 <212> TYPE: DNA  
24 <213> ORGANISM: Homo sapiens  
26 <220> FEATURE:  
27 <221> NAME/KEY: CDS  
28 <222> LOCATION: (12)..(1400)  
30 <400> SEQUENCE: 1  
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33 1 5 10  
35 ccc aga tgg gtc ctg tcc cag gtt cag cta cag cag tgg ggc gca gga 98  
36 Pro Arg Trp Val Leu Ser Gln Val Gln Leu Gln Trp Gly Ala Gly  
37 15 20 25  
39 ctg ttg aag cct tcg gag acc ctg tcc acc tgc gct gtc tat ggt 146  
40 Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly  
41 30 35 40 45  
43 ggg tcc ttc agt ggt tac tac tgg acc tgg atc cgc cag ccc cca ggg 194  
44 Gly Ser Phe Ser Gly Tyr Tyr Trp Thr Trp Ile Arg Gln Pro Pro Gly  
45 50 55 60  
47 aag ggg ctg gag tgg att ggg gaa atc att cat cat gga aac acc aac 242  
48 Lys Gly Leu Glu Trp Ile Gly Glu Ile Ile His His Gly Asn Thr Asn  
49 65 70 75  
51 tac aac ccg tcc ctc aag agt cga gtc tcc ata tca gtt gac acg tcc 290  
52 Tyr Asn Pro Ser Leu Lys Ser Arg Val Ser Ile Ser Val Asp Thr Ser  
53 80 85 90  
55 aag aac cag ttc tcc ctg aca ctg agc tct gtg acc gcc gcg gac acg 338  
56 Lys Asn Gln Phe Ser Leu Thr Leu Ser Ser Val Thr Ala Ala Asp Thr  
57 95 100 105  
59 gct gtg tat tac tgt gcg aga ggg gga gca gtg gct gcg ttt gac tac 386  
60 Ala Val Tyr Tyr Cys Ala Arg Gly Gly Ala Val Ala Ala Phe Asp Tyr

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61	110	115	120	125													
63	tgg	ggc	cag	gga	acc	ctg	gtc	acc	gtc	tcc	tca	gcc	tcc	acc	aag	ggc	434
64	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	
65						130				135					140		
67	cca	tcg	gtc	ttc	ccc	ctg	gcg	ccc	tgc	tcc	agg	agc	acc	tcc	gag	agc	482
68	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	
69											145				155		
71	aca	gcg	gcc	ctg	ggc	tgc	ctg	gct	aag	gac	tac	ttc	ccc	gaa	ccg	gtg	530
72	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	
73											160			165		170	
75	acg	gtg	tcg	tgg	aac	tca	ggc	gct	ctg	acc	agc	ggc	gtg	cac	acc	ttc	578
76	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	
77											175			180		185	
79	cca	gct	gtc	cta	cag	tcc	tca	gga	ctc	tac	tcc	ctc	agc	agc	gtg	gtg	626
80	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	
81											190			195		200	205
83	acc	gtg	ccc	tcc	agc	aac	ttc	ggc	acc	cag	acc	tac	acc	tgc	aac	gta	674
84	Thr	Val	Pro	Ser	Ser	Asn	Phe	Gly	Thr	Gln	Thr	Tyr	Thr	Cys	Asn	Val	
85											210			215		220	
87	gat	cac	aag	ccc	agc	aac	acc	aag	gtg	gac	aag	aca	gtt	gag	cgc	aaa	722
88	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Thr	Val	Glu	Arg	Lys	
89											225			230		235	
91	tgt	tgt	gtc	gag	tgc	cca	ccg	tgc	cca	gca	cca	cct	gtg	gca	gga	ccg	770
92	Cys	Cys	Val	Glu	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Pro	Val	Ala	Gly	Pro	
93											240			245		250	
95	tca	gtc	ttc	ctc	ttc	ccc	cca	aaa	ccc	aag	gac	acc	ctc	atg	atc	tcc	818
96	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	
97											255			260		265	
99	cg	acc	cct	gag	gtc	acg	tgc	gtg	gtg	gac	gtg	agc	cac	gaa	gac	866	
100	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	
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103	ccc	gag	gtc	cag	ttc	aac	tgg	tac	gtg	gac	ggc	gtg	gag	gtg	cat	aat	914
104	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	
105											290			295		300	
107	gcc	aag	aca	aag	cca	ccg	gag	gag	cag	ttc	aac	agc	acg	ttc	cgt	gtg	962
108	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Phe	Arg	Val	
109											305			310		315	
111	gtc	agc	gtc	ctc	acc	gtt	gtg	cac	cag	gac	tgg	ctg	aac	ggc	aag	gag	1010
112	Val	Ser	Val	Leu	Thr	Val	Val	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	
113											320			325		330	
115	tac	aag	tgc	aag	gtc	tcc	aac	aaa	ggc	ctc	cca	gcc	ccc	atc	gag	aaa	1058
116	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ala	Pro	Ile	Glu	Lys	
117											335			340		345	
119	acc	atc	tcc	aaa	acc	aaa	ggg	cag	ccc	cga	gaa	cca	cag	gtg	tac	acc	1106
120	Thr	Ile	Ser	Lys	Thr	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	
121											350			355		360	365
123	ctg	ccc	cca	tcc	ccg	gag	gag	atg	acc	aag	aac	cag	gtc	agc	ctg	acc	1154
124	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	
125											370			375		380	

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127	tgc	ctg	gtc	aaa	ggc	ttc	tac	ccc	agc	gac	atc	gcc	gtg	gag	tgg	gag	1202
128	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	
129				385					390					395			
131	agc	aat	ggg	cag	ccg	gag	aac	aac	tac	aag	acc	aca	cct	ccc	atg	ctg	1250
132	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Met	Leu	
133					400			405			410						
135	gac	tcc	gac	ggc	tcc	ttc	ttc	ctc	tac	agc	aag	ctc	acc	gtg	gac	aag	1298
136	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	
137					415			420			425						
139	agc	agg	tgg	cag	cag	ggg	aac	gtc	ttc	tca	tgc	tcc	gtg	atg	cat	gag	1346
140	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	
141					430			435			440			445			
143	gct	ctg	cac	aac	cac	tac	acg	cag	aag	agc	ctc	tcc	ctg	tct	ccg	ggt	1394
144	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	
145						450			455			460					
147	aaa	tga	gtgccacggc	cgccaagccc	ccgctccccca	ggctctcggg	gtcgctgag										1450
148	Lys																
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162	Val	Leu	Ser	Gln	Val	Gln	Leu	Gln	Gln	Trp	Gly	Ala	Gly	Leu	Leu	Lys	
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165	Pro	Ser	Glu	Thr	Leu	Ser	Leu	Thr	Cys	Ala	Val	Tyr	Gly	Gly	Ser	Phe	
166					35			40			45						
168	Ser	Gly	Tyr	Tyr	Trp	Trp	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	Gly	Leu	
169					50			55			60						
171	Glu	Trp	Ile	Gly	Glu	Ile	Ile	His	His	Gly	Asn	Thr	Asn	Tyr	Asn	Pro	
172		65				70			75			80					
174	Ser	Leu	Lys	Ser	Arg	Val	Ser	Ile	Ser	Val	Asp	Thr	Ser	Lys	Asn	Gln	
175						85			90			95					
177	Phe	Ser	Leu	Thr	Leu	Ser	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Val	Tyr	
178					100			105			110						
180	Tyr	Cys	Ala	Arg	Gly	Gly	Ala	Val	Ala	Ala	Phe	Asp	Tyr	Trp	Gly	Gln	
181					115			120			125						
183	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	
184					130			135			140						
186	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	
187		145				150			155			160					
189	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	
190					165				170			175					
192	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	
193					180				185			190					
195	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Val	Thr	Val	Pro
196					195			200			205						

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198 Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys  
199 210 215 220  
201 Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val  
202 225 230 235 240  
204 Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe  
205 245 250 255  
207 Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro  
208 260 265 270  
210 Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val  
211 275 280 285  
213 Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr  
214 290 295 300  
216 Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val  
217 305 310 315 320  
219 Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys  
220 325 330 335  
222 Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser  
223 340 345 350  
225 Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro  
226 355 360 365  
228 Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val  
229 370 375 380  
231 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly  
232 385 390 395 400  
234 Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp  
235 405 410 415  
237 Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp  
238 420 425 430  
240 Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His  
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248 <211> LENGTH: 23  
249 <212> TYPE: DNA  
250 <213> ORGANISM: Artificial Sequence  
252 <220> FEATURE:  
253 <223> OTHER INFORMATION: Description of Artificial Sequence:Artificially  
254 synthesized primer sequence, HG2-3-437  
256 <400> SEQUENCE: 3  
257 gtgttaggtct gggtgccgaa gtt 23  
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261 <211> LENGTH: 23  
262 <212> TYPE: DNA  
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267 synthesized primer sequence, VH4-21  
269 <400> SEQUENCE: 4

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275 <212> TYPE: DNA  
276 <213> ORGANISM: Artificial Sequence  
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279 <223> OTHER INFORMATION: Description of Artificial Sequence:Artificially  
280 synthesized primer sequence, CG2-1  
282 <400> SEQUENCE: 5  
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**VERIFICATION SUMMARY**  
PATENT APPLICATION: **US/09/937,495**

DATE: 02/02/2005  
TIME: 16:16:50

**Input Set : E:\seqlist.txt**  
**Output Set: N:\CRF4\02022005\I937495.raw**

L:11 M:270 C: Current Application Number differs, Replaced Current Application No  
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date